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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 16:43:55 ; Search time 12994 Seconds
(without alignments)
12072.116 Million cell updates/sec

Title: US-09-715-927-7

Perfect score: 7496

Sequence: 1 agctgctcaggcgctccgc.....gttgagcatggagaaaaaa 7496

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
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- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
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- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match Length | ID | Description |
|------------|-------|--------------|----|-------------|
| ----- | | | | |

| C | 1 | 3113 | 41.5 | 167891 | 9 | AC013439 | AC013439 Homo sapi |
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| | 3 | 653 | 8.7 | 67729 | 2 | AC073035 | AC073035 Homo sapi |
| | 4 | 647.6 | 8.6 | 2222 | 9 | AF226614 | AF226614 Homo sapi |
| | 5 | 647.6 | 8.6 | 2824 | 6 | AX188313 | AX188313 Sequence |
| | 6 | 647.6 | 8.6 | 3081 | 6 | AX047362 | AX047362 Sequence |
| | 7 | 647.6 | 8.6 | 3333 | 6 | AX086462 | AX086462 Sequence |
| | 8 | 647.6 | 8.6 | 3333 | 9 | HS0801908 | AL136944 Homo sapi |
| | 9 | 646 | 8.6 | 2443 | 9 | AF231121 | AF231121 Homo sapi |
| | 10 | 641.2 | 8.6 | 3317 | 9 | AF215636 | AF215636 Homo sapi |
| | 11 | 637.4 | 8.5 | 62947 | 2 | AC083764 | AC083764 Homo sapi |
| | 12 | 633.6 | 8.5 | 2286 | 9 | AK002038 | AK002038 Homo sapi |
| | 13 | 513 | 6.8 | 513 | 9 | AF147322 | AF147322 Homo sapi |
| | 14 | 488.8 | 6.5 | 172437 | 2 | AC096437 | AC096437 Rattus no |
| | 15 | 475.8 | 6.3 | 1949 | 10 | AF394785 | AF394785 Rattus no |
| | 16 | 460 | 6.1 | 2129 | 10 | RRU76714 | U76714 Rattus norv |
| | 17 | 453 | 6.0 | 2111 | 10 | AF215637 | AF215637 Mus muscu |
| | 18 | 453 | 6.0 | 2130 | 10 | AF226613 | AF226613 Mus muscu |
| | 19 | 453 | 6.0 | 3273 | 10 | BC003438 | BC003438 Mus muscu |
| | 20 | 452.6 | 6.0 | 3304 | 10 | AF231120 | AF231120 Mus muscu |
| | 21 | 416.2 | 5.6 | 74673 | 2 | AC027814 | AC027814 Homo sapi |
| | 22 | 337 | 4.5 | 486 | 6 | AX187577 | AX187577 Sequence |
| | 23 | 337 | 4.5 | 527 | 6 | AX184710 | AX184710 Sequence |
| | 24 | 337 | 4.5 | 628 | 6 | AX186515 | AX186515 Sequence |
| | 25 | 282 | 3.8 | 166526 | 2 | AC079209 | AC079209 Homo sapi |
| | 26 | 279.8 | 3.7 | 177720 | 9 | AC019193 | AC019193 Homo sapi |
| | 27 | 279.8 | 3.7 | 183245 | 2 | AC099397 | AC099397 Homo sapi |
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| | 29 | 279.4 | 3.7 | 182312 | 2 | AC099056 | AC099056 Homo sapi |
| | 30 | 278.4 | 3.7 | 154792 | 2 | AC108111 | AC108111 Homo sapi |
| | 31 | 278 | 3.7 | 44327 | 9 | HS0277557 | AX277557 Homo sapi |
| | 32 | 278 | 3.7 | 93713 | 9 | AC006071 | AC006071 Homo sapi |
| | 33 | 278 | 3.7 | 95456 | 2 | AC002092 | AC002092 Homo sapi |
| | 34 | 277.8 | 3.7 | 88484 | 9 | AL355794 | AL355794 Human DNA |
| | 35 | 276.8 | 3.7 | 130964 | 9 | AP000609 | AP000609 Homo sapi |
| | 36 | 276.8 | 3.7 | 183085 | 9 | AC005815 | AC005815 Homo sapi |
| | 37 | 276.6 | 3.7 | 157985 | 9 | CNS05TBM | AL163853 Human Chr |
| | 38 | 276.6 | 3.7 | 203790 | 9 | AC010422 | AC010422 Homo sapi |
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| | 40 | 276.2 | 3.7 | 156100 | 2 | AC011934 | AC011934 Homo sapi |
| | 41 | 276 | 3.7 | 12619 | 6 | AX239606 | AX239606 Sequence |
| | 42 | 276 | 3.7 | 185832 | 9 | AL137800 | AL137800 Human DNA |
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| | 44 | 275.8 | 3.7 | 400 | 11 | GI1389 | GI1389 SHGC-10164 |
| | 45 | 275.8 | 3.7 | 435 | 6 | AX333915 | AX333915 Sequence |

ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens BAC clone Rp11-270G18 from 2, complete sequence.
ACCESSION AC013439
VERSION AC013439.11 GI:13270751
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167891)

Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE 2 (bases 1 to 167891)

Nguyen, C., Cotton, M., Hawkins, M. and Spalding, L.
The sequence of Homo sapiens BAC clone Rp11-270G18
Unpublished
JOURNAL
REFERENCE 3 (bases 1 to 167891)
AUTHORS Waterston, R. H.
TITLE Direct Submission

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JOURNAL Submitted (11-NOV-1999) Genome Sequencing Center, Washington
REFERENCE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
AUTHORS MO 63108, USA
TITLE Waterston,R.
JOURNAL Direct Submission
REFERENCE Submitted (09-AUG-2001) Department of Genetics, Washington
AUTHORS University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
TITLE 5 (bases 1 to 167891)
JOURNAL Waterston,R.
COMMENT Direct Submission
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0270G18
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NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC068833; the clone sequenced to
the right is RP11-88120, 200 bp overlap. Actual start of this
clone is at base position 1 of RP11-270G18; actual end is at base
position 167891 of RP11-270G18.
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Best Local Similarity 86.8%; Pred. No. 0;
Matches 3664; Conservative 0; Mismatches 115; Indels 442; Gaps 4;

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| Db 126048 | TGGCTCCAAATCCTGAAGCTTTTGGCTTGCTCGTATTGATTTTCAGTCTCCTTTGTGGCAA | 125989 |
| Qy 7176 | tgggccaattatgtattttccgatttgcgaataactctgggaaacaagctctttgttgc | 7235 |
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| Db 125748 | AGAACTAAAAGCTGTGTTAGGAAACCTTAAGTCAGCAGAAATTAAGTGAATTTCCCTTA | 125689 |
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| AC073035/c | | |
| LOCUS | 67729 bp | DNA linear HTG 08-JUN-2000 |
| DEFINITION | Homo sapiens chromosome 2 clone RP11-38301 map 2, LOW-PASS SEQUENC | |
| | SAMPLING. | |
| ACCESSION | AC073035 | |
| VERSION | AC073035.1 | GI:8347978 |
| KEYWORDS | HTG; HTGS_PHASE0. | |
| SOURCE | human. | |
| ORGANISM | Homo sapiens | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| REFERENCE | 1 (bases 1 to 67729) | |
| AUTHORS | Blirren,B., Linton,L., Nusbaum,C. and Lander,E. | |
| TITLE | Homo sapiens chromosome 2, clone RP11-38301 | |
| JOURNAL | unpublished | |
| REFERENCE | 2 (bases 1 to 67729) | |
| AUTHORS | Blirren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allien,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F., Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Callumore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galand-Jerre,N., Grant,G., Guyette,M., Graham,L., Grand-pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGuck,A., McKernan,K., McPheeters,R., Melgrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severi,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M. | |
| TITLE | Direct Submission | |
| JOURNAL | Submitted (08-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | |
| COMMENT | All repeats were identified using RepeatMasker. | |


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AC073035      AC073035      67729 bp      DNA      linear      HTG 08-JUN-2000
LOCUS      Homo sapiens chromosome 2 clone RP11-38301 map 2, LOW-PASS SEQUENCE
DEFINITION      SAMPLING.
ACCESSION      AC073035
VERSION      AC073035.1 GI:8347978
KEYWORDS      HTG; HTGS-PHASE0.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 67729)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
               Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
               Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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               Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
               Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
               Young,G., Zainoun,J., Zimmer,A. and Zody,M.
               Direct Submission
               Submitted (08-JUN-2000) Whitehead Institute/MIT Center for Genome
               Research, 320 Charles Street, Cambridge, MA 02141, USA
               All repeats were identified using RepeatMasker:
               Smit, A.F.A. & Green, P. (1996-1997)
               http://ftp.genome.washington.edu/RM/RepeatMasker.html
               ----- Genome Center
               Center: Whitehead Institute/ MIT Center for Genome Research
               Center code: WIBR
               Web site: http://www.seq.wi.mit.edu
               Contact: sequence_submissions@genome.wi.mit.edu
               ----- Project Information
               Center project name: LI0434
               Center clone name: 383_O_1
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               * NOTE: This record contains 78 individual
               * sequencing reads that have not been assembled into
               * contigs. Runs of N are used to separate the reads
               * and the order in which they appear is completely
               * arbitrary. Low-pass sequence sampling is useful for
               * identifying clones that may be gene-rich and allows
               * overlap relationships among clones to be deduced.
               * However, it should not be assumed that this clone
               * will be sequenced to completion. In the event that
               * the record is updated, the accession number will
               * be preserved.
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               * 881      1643: contig of 763 bp in length
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               * 4359 5217: contig of 759 bp in length
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               * 27871 28635: contig of 765 bp in length
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               * 30367 30466: gap of 100 bp
               * 30467 31248: contig of 782 bp in length
               * 31249 31348: gap of 100 bp
               * 31349 32125: contig of 777 bp in length
               * 32126 32225: gap of 100 bp
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               * 32979 33078: gap of 100 bp
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               * 33866 33965: gap of 100 bp
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               * 35594 35693: gap of 100 bp
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[illegible]


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Db 1775 GTCCCTTTGATTAAGTGTGACACAGTGTGCTGCAAGAAATGTAATGAATCGAAGAGG 1834
Qy 6095 attaataaatgatcgaatgttccctaaa 6124
Db 1835 CATTATAAATGGTGTACAGAACTCCATGAA 1864

RESULT 6
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LOCUS AX047362
DEFINITION Sequence 48 from Patent WO0068380.
ACCESSION AX047362
VERSION AX047362.1 GI:11876608
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3081)
AUTHORS Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baughn,M.R.,
Lu,D.A. and Azimzal,Y.
TITLE Extracellular matrix and adhesion-associated proteins
JOURNAL Patent: WO 0068380-A 48 16-NOV-2000;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 91.5%; Pred. No. 2.9e-117;
Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 5375 ttcttaacagatactgagccaaacccctggagggaactcatctaatgggtgtgaaaga 5434
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Db 1210 GCCCTTCGCTACCTCCAGATGGATGGGTCTCCTACTACAAACAGCCTGTGTTCTGGC 1269
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LOCUS AX086462
DEFINITION Sequence 414 from Patent WO0112659.
ACCESSION AX086462
VERSION AX086462.1 GI:13275974
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3333)
AUTHORS Wiemann,S.
TITLE Human dna sequences
JOURNAL Patent: WO 0112659-A 414 22-FEB-2001;
German Human Genome Project (DE)
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Best Local Similarity 91.5%; Pred. No. 2.8e-117;
Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 5375 ttcttaacagatactgagccaaacccctggagggaactcatctaatgggtgtgaaaga 5434
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LOCUS Homo sapiens mRNA; cDNA DKFp586J0624 (from clone DKFp586J0624);
DEFINITION complete cds.
ACCESSION AL136944
VERSION AL136944.1 GI:12053382
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3333)
AUTHORS Wiemann,S., Well,B., Wellenreuther,R., Gassenhuber,J., Glassl,S.,
Ansorge,W., Boecker,H., Bloeker,H., Bauersachs,S., Blum,H.,
Lauber,J., Duesterhoeft,A., Beyer,A., Koehler,K., Strack,N.,
Mewes,H.W., Ottenwaelder,B., Obermaier,B., Tampe,J., Heubner,D.,
Wambutt,R., Korn,B., Klein,M. and Poustka,A.
Toward a Catalog of Human Genes and Proteins: Sequencing and
Analysis of 500 Novel Complete Protein Coding Human cDNAs
Genome Res. 11 (3), 422-435 (2001)
11230166
2 (bases 1 to 3333)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
Direct Submission
Submitted (18-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of Qiagen (Hilden/Germany) Project.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
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/map="939,9 cR from top of Chr2 linkage group"
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BASE COUNT 931 a 671 c 697 g 1034 t
ORIGIN

Query Match 8.6%; Score 647.6; DB 9; Length 3333;
Best Local Similarity 91.5%; Pred. No. 2.8e-117;
Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 5375 ttcttaacagatactagcacaacccctggaggactcatctaatcgggtggaaga 5434
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QY 5675 tataactgggaataatgggaactgtagcttttacttgctacgctcgaataatgtgttctggt 5734
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QY 5735 tcggacaggctctgatctcaggattggcacagcttctcgtttgatctctgtgtgatctc 5794
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QY 5795 tgtattcatccttgggaagccccctggactgtccgtttctctcttcttgaagatatccgac 5854
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RESULT 9
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 LOCUS Homo sapiens iron-regulated transporter IREG1 (IREG1) mRNA,
 complete cds.
 ACCESSION AF231121
 VERSION AF231121.1 GI:7264728
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2443)
 AUTHORS McKie,A.T., Marciani,P., Rolfs,A., Brennan,K., Wehr,K., Barrow,D.,
 Miret,S., Bomford,A., Peters,T.J., Farzaneh,F., Hediger,M.A.,
 Hentze,M.W. and Simpson,R.J.
 TITLE A novel duodenal iron-regulated transporter, IREG1, implicated in
 the basolateral transfer of iron to the circulation
 JOURNAL Mol. Cell 5 (2), 299-309 (2000)
 MEDLINE 20337919
 REFERENCE 2 (bases 1 to 2443)
 AUTHORS McKie,A.T.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-2000) Molecular Medicine, King's College London,
 Guy's, King's and St. Thomas' Medical School, Rayne Institute 123
 Coldharbour Lane, London SE5 9NU, UK
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 REFERENCE 1 (bases 1 to 3317)
 AUTHORS Abboud,S. and Haile,D.J.
 TITLE A novel mammalian iron-regulated protein involved in intracellular
 iron metabolism
 JOURNAL J. Biol. Chem. 275 (26), 19906-19912 (2000)

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MEDLINE 20347902
REFERENCE 2 (bases 1 to 3317)
AUTHORS Haile,D.J.
TITLE Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to
human chromosome 2q32 by in situ hybridization
JOURNAL Cytogenet. Cell Genet. 88 (3-4), 328-329 (2000)
MEDLINE 20291023
PUBMED 10828623
REFERENCE 3 (bases 1 to 3317)
AUTHORS Haile,D.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-1999) Medicine, UTHSCSA, 7703 Floyd Curl Drive,
San Antonio, TX 78240, USA
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REFERENCE 1 (bases 1 to 62947)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone CTD-2054E23
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 62947)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bieda,F., Boguslavsky,L.,
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Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu

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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10999
Center clone name: 2054_E_23

* NOTE: This record contains 75 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
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VERSION AK002038.1 GI:7023677
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              Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
              Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
              Nakamura,Y., Nagahari,K., Masuho,Y., Niinomiya,K. and Iwayanagi,T.
              NEDO human cDNA sequencing project
              Unpublished
              2 (bases 1 to 2286)
              Isogai,T. and Otsuki,T.
              Direct Submission
              Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
              Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
              (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
              NEDO human cDNA sequencing project supported by Ministry of
              International Trade and Industry of Japan; cDNA full insert
              sequencing: Research Association for Biotechnology; cDNA library
              construction, 5'- & 3'-end one pass sequencing and clone selection:
              Helix Research Institute (supported by Japan Key Technology Center
              etc.) and Department of Virology, Institute of Medical Science,
              University of Tokyo.
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               Matches 684; Conservative 0; Mismatches 64; Indels 2; Gaps 1;

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RESULT 13
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LOCUS Homo sapiens full length insert cDNA clone YB21H04.
DEFINITION AF147322
ACCESSION AF147322
VERSION AF147322.1 GI:4761673
KEYWORDS FLI_CDNA.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behmer,K., Hillier,L.,
Wilson,R. and Waterston,R.
Full Clone Sequencing of the Longest Available Member from Each
UniGene Cluster
Unpublished
2 (bases 1 to 513)
Waterston,R.
Direct Submission
Submitted (30-APR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
```

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the

full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

similar to Arabidopsis thaliana protein AAC28758 (PID:g3395426) (AC004683) unknown protein

The location of this clone is unknown.

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BASE COUNT  142 a  94 c  105 g  172 t
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RESULT 14

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LOCUS Rattus norvegicus clone CH230-145018, *** SEQUENCING IN PROGRESS
***, 59 unordered pieces.
AC096437 3 GI:17947216
VERSION HTG; HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 172437)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunga,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
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Chen,Z., Chowdry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
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Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N.,
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Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 172437)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17062250.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GF00
Center clone name: CH230-145018
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 144276 bases at least Q40

Consensus quality: 151836 bases at least Q30
Consensus quality: 158483 bases at least Q20
Estimated insert size: 150873; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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13794: contig of 7716 bp in length
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30603: gap of unknown length
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43142: gap of unknown length
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43242: gap of unknown length
47940: gap of unknown length
47941: contig of 3858 bp in length
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51798: contig of 5864 bp in length
51799: gap of unknown length
51898: contig of 6875 bp in length
51899: gap of unknown length
57762: contig of 6875 bp in length
57763: gap of unknown length
64737: gap of unknown length
64738: gap of unknown length
64850: contig of 3813 bp in length
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68751: contig of 3263 bp in length
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72114: contig of 3954 bp in length
76068: gap of unknown length
76167: contig of 2748 bp in length
78915: gap of unknown length
79016: contig of 3747 bp in length
82762: gap of unknown length
82763: contig of 2235 bp in length
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85097: contig of 1973 bp in length
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87170: gap of unknown length
87171: contig of 2535 bp in length
87271: gap of unknown length
89806: contig of 1986 bp in length
89905: gap of unknown length
92455: contig of 2550 bp in length
92456: gap of unknown length
95951: contig of 3396 bp in length
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RESULT 15

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VERSION AF394785.1 GI:15021656
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SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1949)
AUTHORS Yeh,K.-Y., Yeh,M. and Glass,J.
TITLE Iron induces ferroportin 1 (FPRT), clustering and redistribution in
rat intestinal epithelial cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1949)
AUTHORS Yeh,K.-Y., Yeh,M. and Glass,J.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2001) Department of Medicine and Feist-Weiller
Cancer Center, Louisiana State University Health Sciences Center,
1501 Kings Highway, Shreveport, LA 71130, USA
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Db 1590 ATCTCCGTCAAGCTGCTGTTTGCAGGAGTCATCTGCTAGAAATCGGCTCTTTGGTCTCTTT 1649
Qy 6042 ttatatataatgaactaaagtgtcttttctgttaagtgtaggttcagagaaatccattata 6101
Db 1650 GATTTGACTGTGACACAGTTCGTGCAAGAAAATGTAATTTGAATCAGAAAGAGGACTTATC 1709
```

Oy 6102 aatgatctgaatgttccctaaa 6124
||| | | | | | | | | |
Db 1710 AATGGTGTGCAGAACTCCATGAA 1732

Search completed: July 23, 2002, 23:47:00
Job time: 25385 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 17:41:00 ; Search time 1026.62 Seconds
(without alignments)
12536.275 Million cell updates/sec

Title: US-09-715-927-7
Perfect score: 7496
Sequence: 1 agctggctcaggcgcctccgc.....qttgagcattcgaaaaaaa 7496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N Genesec 032802.*

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|------------------------|
| 1 | 647.6 | 8.6 | 1861 | 20 | AA590442 | Human secreted protein |
| 2 | 647.6 | 8.6 | 1861 | 22 | AA559271 | Human cDNA encoding |
| 3 | 647.6 | 8.6 | 1861 | 24 | AB450940 | Human polynucleotide |
| 4 | 647.6 | 8.6 | 2824 | 22 | AAH72731 | Human cervical cancer |
| 5 | 647.6 | 8.6 | 3081 | 22 | AA566912 | Human EXMAD-23 coding |
| c | 647.6 | 8.6 | 3328 | 22 | AA160070 | Human polynucleotide |
| 6 | 647.6 | 8.6 | 3454 | 22 | AA158290 | Human polynucleotide |
| 7 | 647.4 | 8.6 | 3420 | 23 | AA584449 | DNA encoding novel |
| c | 636 | 8.5 | 741 | 22 | AA123132 | Human breast cancer |

| | | | | | | |
|----|-------|-----|-------|----|-----------|----------------------|
| 10 | 633.6 | 8.5 | 2286 | 22 | AAH15006 | Human cDNA sequenc |
| 11 | 624.6 | 8.3 | 1540 | 19 | AAS59631 | Human secreted pro |
| 12 | 612.4 | 8.2 | 683 | 22 | AAH07857 | Human cDNA clone (|
| 13 | 609 | 8.1 | 774 | 22 | AAAL21721 | Human breast cancer |
| 14 | 599.8 | 8.0 | 2196 | 19 | AAS59782 | Human secreted pro |
| 15 | 537.2 | 7.2 | 657 | 22 | AAAL14260 | Human breast cancer |
| 16 | 485.4 | 6.5 | 793 | 22 | AAI197641 | Human neuroblastom |
| 17 | 376.6 | 5.0 | 380 | 21 | AAC00628 | Human secreted pro |
| 18 | 338.6 | 4.5 | 725 | 22 | AAAL12850 | Human breast cancer |
| 19 | 337 | 4.5 | 487 | 22 | AAH171997 | Human cervical can |
| 20 | 337 | 4.5 | 527 | 22 | AAH69131 | Human cervical can |
| 21 | 337 | 4.5 | 628 | 22 | AAH70936 | Human cervical can |
| 22 | 276 | 3.7 | 12619 | 22 | AAH26493 | Human low density |
| 23 | 275.8 | 3.7 | 630 | 22 | AAAL23112 | Human breast cancer |
| 24 | 272.8 | 3.6 | 23432 | 22 | AAS35832 | Human cardiovascular |
| 25 | 271.4 | 3.6 | 31949 | 22 | AAAL05410 | Human reproductive |
| 26 | 271.4 | 3.6 | 32186 | 22 | AAAL05411 | Human reproductive |
| 27 | 270 | 3.6 | 1661 | 22 | ABA20581 | Human nervous syst |
| 28 | 270 | 3.6 | 1661 | 22 | ABA20582 | Human nervous syst |
| 29 | 269.8 | 3.6 | 2272 | 22 | ABA07732 | Human ovarian and |
| 30 | 269.8 | 3.6 | 2272 | 22 | AAAL02963 | Human reproductive |
| 31 | 269.2 | 3.6 | 2331 | 22 | AAK066148 | Human immune/haema |
| 32 | 269 | 3.6 | 1516 | 22 | AAH18733 | Human cDNA sequenc |
| 33 | 269 | 3.6 | 2635 | 22 | AAK65774 | Human immune/haema |
| 34 | 269 | 3.6 | 25012 | 22 | AAAL15431 | Human nervous syst |
| 35 | 269 | 3.6 | 27483 | 22 | AAAL36563 | Human musculoskele |
| 36 | 268.4 | 3.6 | 2563 | 22 | AAAL05707 | Human reproductive |
| 37 | 268.4 | 3.6 | 3495 | 21 | AAAG12628 | Human secreted pro |
| 38 | 268.2 | 3.6 | 5671 | 22 | ABAL19206 | Human nervous syst |
| 39 | 268.2 | 3.6 | 5671 | 22 | AAK97076 | Human immune/haema |
| 40 | 268 | 3.6 | 14636 | 22 | AAF31864 | Human DNA-PKcs cod |
| 41 | 267.8 | 3.6 | 3407 | 22 | AAS39882 | Genomic sequence # |
| 42 | 267.8 | 3.6 | 3407 | 22 | AAK902223 | Human digestive syst |
| 43 | 267.8 | 3.6 | 32216 | 22 | ABAL16118 | Human nervous syst |
| 44 | 267.8 | 3.6 | 46553 | 22 | AAK67926 | Human immune/haema |
| 45 | 267.8 | 3.6 | 46553 | 22 | AAK91745 | Human immune/haema |

ALIGNMENTS

| | | |
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| AAAX90442 | | |
| ID | AAAX90442 standard; cDNA; 1861 BP. | |
| XX | | |
| XX | AAAX90442; | |
| XX | | |
| 29-SEP-1999 | (first entry) | |
| XX | | |
| XX | Human secreted protein clone ew150_1 nucleotide sequence | |
| DE | | |
| XX | | |
| KW | Human; secreted protein; nutrition; cytokine; cell proliferation; immune stimulating; vaccine; suppression | |
| KW | haematopoiesis regulation; tissue growth; activin; inhib | |
| KW | chemotactic; chemokinetic; haemostatic; thrombolytic; ant | |
| KW | tumour invasion suppressor; tumour inhibition; ss. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| Key | Location/Qualifiers | |
| CDS | 26..1741 | |
| FT | /*tag= a | |
| FT | /product= "secreted protein" | |
| FT | /transl_except= (pos:629..631,aa:Xaa) | |
| FT | /transl_except= (pos:1535..1537,aa:Xaa) | |
| FT | /note= "Xaa= unknown" | |
| XX | | |
| XX | WO937674-A1. | |
| PN | | |
| XX | | |
| XX | | |
| PD | 29-JUL-1999. | |
| XX | | |
| XX | 21-JAN-1999; | |
| XX | 99WO-US01404. | |
| XX | | |

| | | | |
|----------|--|---|------|
| Db | 1435 | gtcctttgatttaactgtgacacagttgtgcaagaaaatgtaattgtaactggaagagg | 1494 |
| Qy | 6095 | attaataaatgatctgaaatgttccctctaaa | 6124 |
| | | | |
| Db | 1495 | cattataaatggtgtacagaactcccatgaa | 1524 |
| RESULT 3 | | | |
| ABA90940 | | | |
| ID | ABA90940 standard; cDNA; 1861 BP. | | |
| XX | ABA90940; | | |
| XX | AC | | |
| XX | AC | | |
| DT | 14-FEB-2002 (first entry) | | |
| XX | Human polynucleotide SEQ ID NO 129. | | |
| DE | Human; clone bG306-7; clone yB8-1; ATCC number 98599; gene therapy; | | |
| XX | immune disorder; bacterial infection; fungal infection; cancer; tumour; | | |
| KW | autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin | | |
| KW | osteoporosis; osteoarthritis; nervous system disorder; neuropathy; | | |
| KW | Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; | | |
| KW | haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnery; | | |
| KW | ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; | | |
| KW | Crohn's disease; cytostatic; anti-inflammatory; immunomodulator; | | |
| KW | neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss. | | |

KW haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulvectomy;
KW ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic;
KW Crohn's disease; cytostatic; anti-inflammatory; immunomodulator;
KW neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
KW

| | | |
|----|--|--|
| XX | Homo sapiens. | |
| OS | | |
| XX | | |
| XX | US2001039335-A1. | |
| PN | | |
| XX | | |
| XX | 08-NOV-2001. | |
| PD | | |
| XX | | |
| XX | 04-DEC-2000; 2000US-0729674. | |
| XX | | |
| XX | 10-APR-1997; 97US-126425P. | |
| PR | 04-DEC-1997; 97US-067454P. | |
| PR | 20-DEC-1997; 97US-068379P. | |
| PR | 02-JAN-1998; 98US-070346P. | |
| PR | 07-JAN-1998; 98US-070643P. | |
| PR | 08-JAN-1998; 98US-070755P. | |
| PR | 13-JAN-1998; 98US-071304P. | |
| PR | 22-JAN-1998; 98US-072134P. | |
| PR | 30-JAN-1998; 98US-073059P. | |
| PR | 18-FEB-1998; 98US-075038P. | |
| PR | 30-MAR-2000; 2000US-0539330. | |
| PR | 23-NOV-1998; 98US-0197886. | |
| XX | | |
| PA | (JACO/) JACOBS K. | |
| PA | (MCCO/) MCCOY J M. | |
| PA | (LAVA/) LAVALLIE E. R. | |
| PA | (COLL/) COLLINS-RACIE L A. | |
| PA | (EVAN/) EVANS C. | |
| PA | (MERB/) MERBERG D. | |
| PA | (TREA/) TREACY M. | |
| PA | (AGOS/) AGOSTINO M J. | |
| PA | (STEL/) STEININGER R J. | |
| PA | (SPAU/) SPAULDING V. | |
| PA | (WONG/) WONG G G. | |
| PA | (CLAR/) CLARK H. | |
| PA | (FECH/) FECHTEL K. | |
| XX | | |
| PI | Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C; | |
| PI | Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V; | |
| PI | Wong GG, Clark H, Fechtel K; | |
| XX | | |
| XX | WPI: 2002-040725/05. | |
| DR | P-PSDB; ABB55762. | |
| DR | | |
| XX | | |
| PT | New secreted proteins and encoding polynucleotides, useful in gene | |
| PT | therapies, particularly for preventing or treating autoimmune | |
| PT | disorders, cancer, graft-versus-host disease, wound, osteoporosis, | |
| PT | stroke or inflammations - | |
| PT | | |

New secreted proteins and encoding polynucleotides, useful in gene PT
PT therapies, particularly for preventing or treating autoimmune PT
disorders, cancer, graft-versus-host disease, wound, osteoporosis, PT
stroke or inflammations -

Qy 5435 ctctaacatccatgagcttgaaatgagcaagagccctactctgtgctcccccagatggctga 5494
Dy 1175 ctctaacatccatgagcttgaaatgagcaagagccctactctgtgctcccccagatggctga 1234
Qy 5495 gccctccgtacctcccgatgagcttgagctctctactatacaccagcctgtgttctgcgc 5554
Dy 1235 gccctccgtacctcccgatgagcttgagctctctactatacaccagcctgtgttctgcgc 1294
Qy 5555 tggcatgggtctgtcttctcttatactgactgtcctggcttgaactgcataccacagcagg 5614
Dy 1295 tggcatgggtctgtcttctcttatactgactgtcctggcttgaactgcataccacagcagg 1354
Qy 5615 gtacgctacactcaggagactgaggttccatcctcactcagttatttgatgggagcactcagc 5674
Dy 1355 gtacgctacactcaggagactgaggttccatcctcactcagttatttgatgggagcactcagc 1414
Qy 5675 tataactgggaataatgggaactgagcttttactgttctactgtcagctcgaaatgtgttgggt 5734
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Qy 5735 tcggacaggtctgactcagagattggcacagctttctctgtttgatcttctgtgtgatctc 5794
Dy 1475 tcggacaggtctgactcagagattggcacagctttctctgtttgatcttctgtgtgatctc 1534
Qy 5795 tgtattcagctcgtggaagcccccgtggaactgtccggtttctccttttgaagatatccgactc 5854
Dy 1535 tgtattcagctcgtggaagcccccgtggaactgtccggtttctccttttgaagatatccgactc 1594
Qy 5855 aaggttcattcaagagagtgtaattacacctaccacagatacctgaaatgtacactgaaat 5914
Dy 1595 aaggttcattcaagagagtgtaattacacctaccacagatacctgaaatgtacactgaaat 1654
Qy 5915 atacatgtctaattgggtcttaattctgctaatttctcccgagacagctcctgaaatctgt 5974
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Qy 6035 atctcttttataattaataaactaaagtctcttttggtaattgagttcagagaatcc 6094
Dy 1775 gtcttggatttaactgtgacacagtgctgctgcaagaaaatgtaattgaaatcgtgaaagagg 1834
Qy 6095 attataaatgatctgaaatgttccctaaa 6124
Dy 1835 cattataaatggtgtacagaactccatgaa 1864

RESULT 5

AAC66912
ID AAC66912 standard; cDNA; 3081 BP.

XX AC AAC66912;

XX DT 27-MAR-2001 (first entry)

XX DE Human EXMAD-23 coding sequence SEQ ID NO: 48.

XX KW Extracellular matrix and adhesion-associated protein; EXMAD; cancer;
XX KW inflammation; reproductive disorder; cardiovascular disorder;
XX KW immune disorder; musculoskeletal disorder; developmental disorder;
XX KW gastrointestinal disorder; cell proliferation disorder; ss.

XX OS Homo sapiens.

XX PN WO200068380-A2.

XX XX 16-NOV-2000.

XX PF 10-MAY-2000; 2000WO-US12811.

XX XX

PR

PR 11-MAY-1999; 99US-0133643.

XX 23-AUG-1999; 99US-0150409.

PA (INCY-) INCYTE GENOMICS INC.

XX Bandman O, Hillman JL, Tang YT, Lal P, Yue H, Baughn MR, Lu DAM;

PI Azimzai Y;

DR WPI; 2001-007395/01.

DR P-PSDB; AAB27245.

XX Isolated polynucleotide encoding extracellular matrix or

PT adhesion-associated protein (EXMAD) useful for diagnosing, treating, or

PT preventing disorders associated with expression of EXMAD such as

PT proliferative, immune and genetic disorders -

XX Claim 4; Page 127-128; 129pp; English.

PS

XX The present invention provides the protein and coding sequences for 25

CC novel extracellular matrix and adhesion-associated proteins (EXMADS).

CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5,

CC EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,

CC EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19,

CC EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are

CC useful in the prevention and treatment of cancers, cell proliferation, and

CC cardiovascular, reproductive, immune, musculoskeletal, developmental and

CC gastrointestinal disorders and inflammation.

XX

SQ Sequence 3081 BP; 829 A; 643 C; 680 G; 929 T; 0 other;

Query Match

Best Local Similarity 8.6%; Score 647.6; DB 22; Length 3081;

Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Dy 1090 tttaacacaaatgactgagccaaacccctggagggaactcactcattggtgtgaaaga 1149

Qy 5435 ctctaaacatccatgagcttgaaatgagcaagagcctactgtgctccagatggctga 5494

Dy 1150 ctctaaacatccatgagcttgaaatgagcaagagcctactgtgctccagatggctga 1209

Qy 5495 gccctccgtacccctccagatgagtggtctcctactacacacagcctgtgttctggc 5554

Dy 1210 gccctccgtacccctccagatgagtggtctcctactacacacagcctgtgttctggc 1269

Qy 5555 tggcatgggtctgtcttctcttatactgactgtcctgggttgaactcaccacagcagg 5614

Dy 1270 tggcatgggtctgtcttctcttatactgactgtcctgggttgaactcaccacagcagg 1329

Qy 5615 gtacgctacactcagggagctgagtggttccatcctcagttatttgatggagatcagc 5674

Dy 1330 gtacgctacactcagggagctgagtggttccatcctcagttatttgatggagatcagc 1389

Qy 5675 tataactgggaataatgggaactgtagcttttacttggctagcgtcgaaatgtgttgggt 5734

Dy 1390 tataactgggaataatgggaactgtagcttttacttggctagcgtcgaaatgtgttgggt 1449

Qy 5735 tcggacaggtctgactcagagattggcacagcttctctgttttgatctctgtgtgatctc 5794

Dy 1450 tcggacaggtctgactcagagattggcacagcttctctgttttgatctctgtgtgatctc 1509

Qy 5795 tgtattcagctcgtggaagcccccgtggaactgtccgtttctccttttgaagatatccgactc 5854

Dy 1510 tgtattcagctcgtggaagcccccgtggaactgtccgtttctccttttgaagatatccgactc 1569

Qy 5855 aaggttcattcaagagagtgtaattacacctaccacagatacctgaaatgtacactgaaat 5914

Dy 1570 aaggttcattcaagagagtgtaattacacctaccacagatacctgaaatgtacactgaaat 1629

Qy 5915 ataatgtctaatgggtcttaattctcgttaattgtcccgagacaaagtctcgtgaatctgt 5974


```
Db 734 GGGAGACCTGGTGAGCCTCCCAACAGCGCTCCATAGGGCTTGCCCTTCACAAATTAAAGTT 675
Qy 87 acagttagtaagtttgaaagaagaaagaaatccctcctggccctttctttt 146
Db 674 ACAGTGTAGCTAAG-TTGGAAAGAAGAAAGAAATCCCTGGGCCCTTTCTTTG 616
Qy 147 gttcttggcaaatcgtcgttgtagctcttttggcccaaggctgtgtgttagaggt 206
Db 615 GTTCTTTGGCAAGTGTGCTGTGTAGTCTTTTTCGCCAGGGCTGTGTGTAAAGGT 556
Qy 207 gctatccagttcttgcactcctgttaacaagcactcagcgagagcagcagcga 266
Db 555 GCTATCTCCAGTTCCTTGACCCCTGTAAACAACACCTCAGCCAGAGACACACGCA 496
Qy 267 tagcagcgcagaagaccagcgggctgcctagctgtcatgaccagggcgagatcaca 326
Db 495 TAGCAGCGCAGAGAAGCCAGCGGGTGCCTAGTGTATGACCGAGGGGAGATCACA 436
Qy 327 accgcaagagagatgctgtgtgtagtgcgttgacccaagacataggtggaaacccag 386
Db 435 ACCGCCAGAGAGGATGCTGTGTGAGTGTGCTTGACCGAAGCATATGGTGGAAACCCAG 376
Qy 387 gtggggctttggacacaagcaactcaccaggtctctggaggaatgtggctctgtga 446
Db 375 GTGGGGCTTTGGAGACAAGCAACTCTACACGAGTCTCGAGGAATGTGGCTCTCTGTGA 316
Qy 447 accatagctttgtaaaagatcctttgactcattttgttggaagcttaaggaagaaagga 506
Db 315 ACCATAGCTTTGTAAAAAGATCCTTTGACTCATATTTTGGTGGAGCTTAAGGAAGAAAGGA 256
Qy 507 aattcagggctggaaaggggtttcacacagcgacggatggatgagattggcagtt 566
Db 255 AATTCAAGGGTGTGGAAAGGGGTTCACACAGGCTCGGATGGAGTAGATTTGGGCAGTT 196
Qy 567 tggattccttgtgtaaaagaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 626
Db 195 TGGATTGCTGTGTAAAAAGAAACAAAA----- 164
Qy 627 aaccaacaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 686
Db 165 ---CAAAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 109
Qy 687 tgaatgtgaattggcagctattgactaggttcactgaggtcaataactgaattgagtgatt 746
Db 108 TGAATGTGAATTGGCAGGTATTGACTAGGTCAATAACTGAATTAGTGAATGGTATT 49
Qy 747 aagtgaacgaataacatcggcttcactaggttaacttgataaaatgtacgt 794
Db 48 AAGTGAACGAATAACATCGGTTTCATAGGTAACCTTGATTAATAATGTACCT 1

RESULT 10
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ID AAH15006 standard; cDNA; 2286 BP.
XX
AC AAH15006;
XX
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:12958.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-011626.
XX
XX 29-JUL-1999; 99JP-0248036.
XX
XX 27-AUG-1999; 99JP-0300253.
PR
```

```
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isozaki T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX Claim 8; SEQ ID 12958; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dr primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
XX AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX Sequence 2286 BP; 678 A; 421 C; 434 G; 753 T; 0 other;
XX
XX Query Match 8.5%; Score 633.6; DB 22; Length 2286;
XX Best Local Similarity 91.2%; Pred. No. 3.9e-106;
XX Matches 684; Conservative 0; Mismatches 64; Indels 2; Gaps 1;
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Db 36 ttacacaagatactagcacaacccctggagggaactcatctaatgggtgaaaga 95
Qy 5435 ctctaatacatcctagcttgacaatgagcagagcctacttgcctcccagatggctga 5494
Db 96 ctctaatacatcctagcttgacaatgagcagagcctacttgcctcccagatggctga 155
Qy 5495 gcccttcctgacttcccgagatggatgggtctcctactactacaacccagcctgtttctggc 5554
Db 156 gcccttcctgacttcccgagatggatgggtctcctactactacaacccagcctgtttctggc 215
Qy 5555 tggcatgggttcttcttcttcttatagctgtcctgggttactgcatcaccaagg 5614
Db 216 tggcatgggttcttcttcttcttatagctgtcctgggttactgcatcaccaagg 275
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Db 276 gtacgctcactcagggactgaggttccatcctcagttatttgaggagcatcagc 335
Qy 5675 tataactggaataaatgggaactgtagcttttacttggctacgtcgaaatgtgttgggt 5734
Db 336 tataactggaataaatgggaactgtagcttttacttggctacgtcgaaatgtgttgggt 395
Qy 5735 tcggacaggtctgatctcagcaggttggaacgcttctctgttattgtgtgatctc 5794
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Qy 5855 aaggttcattcaagagagagtgcaattacacacctaccacatacctgaaattacaactgaaat 5914
Db 516 aaggttcattcaagagagtgcaattacacacctaccacatacctgaaattacaactgaa-- 573
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Qy 6035 atctcttttatatatataatgaactaaagtgctctttttgtaatgtaggttcagagaatacc 6094
Db 694 gtcctttgatttaactgtgacacagttgtgcagaataatgtaattgaatcctgaaagagg 753
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RESULT 11
AAV59651
ID AAV59651 standard; DNA; 1540 BP.
XX
AC AAV59651;
XX
DF 19-JAN-1999 (first entry)
XX
DE Human secreted protein gene 141 clone HCM530.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
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PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
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PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
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PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
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PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
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PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
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PR 22-AUG-1997; 97US-0056875.
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PR 22-AUG-1997; 97US-0056877.
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PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
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PR 22-AUG-1997; 97US-0056903.
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PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057659.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Peng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 DR WPI; 1998-506364/43.
 DR P-PSDB; AAW74869.
 DR
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 375-376; 721pp; English.
 XX
 CC This sequence represents a nucleic acid molecule designated Gene 141
 CC from the human cDNA clone HCM5H30 (deposited as clone ATCC 97902 and
 CC ATCC 209048) which encodes a secreted human protein. The gene can be
 CC used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 XX
 SQ Sequence 1540 BP; 404 A; 325 C; 343 G; 466 T; 2 other;

Query Match 8.3%; Score 624.6; DB 19; Length 1540;
 Best Local Similarity 91.2%; Pred. NO. 1.6e-104;
 Matches 685; Conservative 0; Mismatches 64; Indels 2; Gaps 2;

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 DB 230 ttacacaaagatgactgagccaaacccctggagggaactcatctaatgggtgtaaga 289
 QY 5435 ctctaacatcatgagcttgaaacatgagcaagcctactgtgctccacagatggctga 5494
 DB 290 ctctaacatcatgagcttgaaacatgagcaagcctactgtgctccacagatggctga 349
 QY 5495 gcccttcgctaccttcgagatgggtgctctactactaacacagcctgtgttctggc 5554
 DB 350 gcccttcgctaccttcgagatgggtgctctactactaacacagcctgtgttctggc 409
 QY 5555 tggcattggcttgccttcttatatgactgctcctgggttgaactacacacagg 5614
 DB 410 tggcattggcttgccttcttatatgactgctcctgggttgaactacacacagg 469
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 DB 470 gtaagcctacactcaggagctgagt-ggtccatccctcagatatttgaatggagcatcag 529
 QY 5674 ctataactggaataaagggaactgtagcttttacttggtcagctcgaaaaatggtgttgg 5733
 DB 530 ctataactggaataaagggaactgtagcttttacttggtcagctcgaaaaatggtgttgg 589
 QY 5734 ttcggacaggctctgatctcaggaattggcacagcttctctgttctgtgtgatct 5793

Db 590 ttcgg-caggtctgatctcaggtattggcacagcttctctgttgatcttctgtgtgatct 648
 QY 5794 ctgtattcatgcttggagccctcctggacttgccttctccttttgaagataccgat 5853
 Db 649 ctgtattcatgcttggagccctcctggacttgccttctccttttgaagataccgat 708
 QY 5854 caaggttcattcaaggagagctcaattacacactacacagatacctgaaattacaactgaaa 5913
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 QY 6034 aatctcttttatataatgaactaaagtgtcttttttgaatgtaggttcagagaatc 6093
 Db 889 ggtccttggatttaactgtgacacagctgtcgtcgaagaaaatgtaattgaatctgaaagag 948
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 ID AAH07857 standard; cDNA; 683 BP.
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 AC AAH07857;
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 DT 26-JUN-2001 (first entry)
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 DE Human cDNA clone (5'-primer) SEQ ID NO:4692.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
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 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 1; SEQ ID 4692; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the

| | | | | | |
|--|----------|-----|---|-----|--|
| | Db | 416 | TGGTGAGTGTCTTGACCGAAAGCATATGGTGGAAACCAGGCTGGGGCTTTGAAGACAAG | 357 | PR 11-APR-1997; PR 11-APR-1997; PR 11-APR-1997; |
| | Oy | 406 | caactctaccgcgagttcttgagggaatgtggctctgtctgtgaacctagtctttaaagaag | 465 | PR 11-APR-1997; PR 11-APR-1997; PR 11-APR-1997; |
| | Db | 356 | CAACTCTACACGAGTTCGTGGAGGAATGTGGCTCTGCTGTGAACCATAGCTTTGTAAAAAG | 297 | PR 11-APR-1997; PR 11-APR-1997; PR 11-APR-1997; |
| | Oy | 466 | atcctttgactcatatttgytggacgtttaagaaagaaaagaaataccaggttgtggaaaaa | 525 | PR 11-APR-1997; PR 11-APR-1997; PR 11-APR-1997; |
| | Db | 296 | ATCCTTTGACTCATATTGTGTGGACGTTAAGGAAGAAGAAAATTCAGGGTGTGGGAAAA | 237 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
| | Oy | 526 | gggttttcacacaggaacgatggatagattgggcagatttggattcccttggtaaaaa | 585 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
| | Db | 236 | GGGGTTTGCCACACAGGCCTCGGATGGAGTAGATGGGCCAGTTGGGATTCCTTGTGTAAAA | 177 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
| | Oy | 586 | aagaacaaacaaacaaaccaaaccaccccg999aaaaaaaaaacaaacaaacaaaccaa | 645 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
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| | Db | 149 | CCCCAAAAAGAAATGTTGAAACAAGAGTTTCTCTACTGTATGTGAATGTGAAGTTGGGCA | 90 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
| | Oy | 706 | gttattactaggtccaataactgaatttagtgaatggttatgaagtgaacgaatacatcog | 765 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
| | Db | 89 | GTTATGTACTAGGTCATAACTGAATTTAGTGAATGGTATTAAAGTGAACGAATACATCG | 30 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
| | Oy | 766 | gttcataagtaacttgataaaatgtacqt | 794 | PR 23-MAY-1997; PR 23-MAY-1997; PR 23-MAY-1997; |
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| | XX | AC | AAV59782; | | |
| | XX | DT | 19-JAN-1999 (first entry) | | |
| | XX | DE | Human secreted protein gene 141 clone HCMSH30. | | |
| | XX | KW | Human; secreted protein; fusion protein; gene therapy; protein therapy; | | |
| | XX | KW | diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; | | |
| | XX | KW | developmental abnormality; foetal deficiency; blood; allergy; renal; ds; | | |
| | XX | KW | immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; | | |
| | XX | KW | inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; | | |
| | XX | KW | cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; | | |
| | XX | KW | osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; | | |
| | XX | OS | endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm. | | |
| | XX | PN | Homo sapiens. | | |
| | XX | PD | WO9839448-A2. | | |
| | XX | PF | 11-SEP-1998. | | |
| | XX | PF | 06-MAR-1998; 98WO-US04493. | | |
| | XX | PR | 02-OCT-1997; 97US-0061060. | | |
| | XX | PR | 07-MAR-1997; 97US-0038621. | | |
| | XX | PR | 07-MAR-1997; 97US-0040161. | | |
| | XX | PR | 07-MAR-1997; 97US-0040162. | | |
| | XX | PR | 07-MAR-1997; 97US-0040163. | | |
| | XX | PR | 07-MAR-1997; 97US-0040334. | | |
| | XX | PR | 07-MAR-1997; 97US-0040336. | | |
| | XX | PR | 07-MAR-1997; 97US-0040626. | | |
| | XX | PR | 11-APR-1997; 97US-0043311. | | |
| | XX | PR | 11-APR-1997; 97US-0043312. | | |
| | XX | PR | 11-APR-1997; 97US-0043313. | | |
| | XX | PR | 11-APR-1997; 97US-0043314. | | |
| | XX | PR | 11-APR-1997; 97US-0043568. | | |

CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
xx
SQ Sequence 657 BP; 165 A; 175 C; 122 G; 192 T; 3 other;

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Query Match          7.28; Score 537.2; DB 22; Length 657;
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Matches 629; Conservative 0; Mismatches 20; Indels 41; Gaps 4;

Qy 113 ggaagaaagaaatccctgggcccc-----tttcttttttcttcccaagtcgctcg 166
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Qy 167 ttgtagtc-ttttgcocaaaggtgtgtgttttttagaggtctatctccagttccctgc 225
Db 597 TTGTAGTCTTTTTCGCCAAGNCCTGTGTGTTTATAGAGTGTCTATCTCCAGTTCCCTTGC 538

Qy 226 act-ccgtttaacagcactcagcagcagcagcagcagcagcagcagcagcagcagcagc 284
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Qy 285 cagcggggtcgctagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 344
Db 477 CAGCGGGTCCGCTAGTGTCTATGACCGGGCGGAGATCACAAACCCAGAGAGGATGCT 418

Qy 345 gtgtgagtcgtcgtgacccaaagcatatgtgtgaaacccaggtgggctttggagacaa 404
Db 417 GTGGTGTAGTGTCTGTACCGAAGCATATGTTGGAAACCCAGGTGGGGCTTTGGAGACAA 358

Qy 405 gcaactctaccggagttctggaggaatgtggctctgtgtgaaccatagcttttataaaa 464
Db 357 GCAACTCTACACGAGTCTTGAGGAATGTGGCTCTGTCTGAACCATAGCTTTGTAAAA 298

Qy 465 gatcctttgactcatattgttgacgttaaggaagaaagaaattcagggtgtgggaaa 524
Db 297 GATCCTTTGACTCATATTTGTGGACGTTAAGGAAGAAAGAAATTCAGGGTGTGGGAAA 238

Qy 525 aggggtttgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 584
Db 237 AGGGGTTTGCACACAGGCTCGGATGGAGTAGATTGGGCAGTTTGGATTGCCCTTGTGTAA 178

Qy 585 aaagaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 644
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Qy 645 acccaaaagaaatgtgaacaaagatttctctctgtatgtgaatgtgaagtgggc 704
Db 150 ACCCAAAAAGAAATGCTGAACACAGAGTTTCTTACCTGTATGTGAAATGTGAAGTTGGGC 91

Qy 705 agttattgactagtgcaataactgaattagtgaaatggatttaagtgaacgaataacatc 764
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Qy 765 ggttcattaggttaactgataaaatgtaagt 794
Db 30 GGTTCATAGGTAAGTGTGATAAAATGTACCT 1
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Job time: 22025 sec

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 16:47:55 ; Search time 205.14 seconds
(without alignments)

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 268 | 3.6 | 14636 | 4 | US-09-173-914-6 | | Sequence 6, Appl |
| 2 | 262.6 | 3.5 | 13158 | 2 | US-08-687-080-105 | | Sequence 105, App |
| 3 | 261.6 | 3.5 | 84495 | 4 | US-09-797-906-3 | | Sequence 3, Appl |
| 4 | 260.2 | 3.5 | 40328 | 3 | US-08-743-185-102 | | Sequence 102, App |
| 5 | 259.2 | 3.5 | 320 | 1 | US-08-620-939-5 | | Sequence 5, Appl |
| 6 | 259.2 | 3.5 | 320 | 1 | US-08-759-873-5 | | Sequence 5, Appl |
| 7 | 259 | 3.5 | 43795 | 3 | US-08-743-185-101 | | Sequence 101, App |
| C 8 | 258.6 | 3.4 | 3742 | 1 | US-08-694-915-5 | | Sequence 5, Appl |
| C 9 | 258 | 3.4 | 246240 | 2 | US-08-724-394A-20 | | Sequence 20, Appl |
| C 10 | 258 | 3.4 | 246240 | 2 | US-08-724-394A-21 | | Sequence 21, Appl |
| C 11 | 258 | 3.4 | 246240 | 2 | US-08-724-394A-22 | | Sequence 22, Appl |
| C 12 | 257.4 | 3.4 | 14796 | 4 | US-08-975-080-35 | | Sequence 35, Appl |
| C 13 | 257.4 | 3.4 | 14796 | 4 | US-09-630-706-10 | | Sequence 10, Appl |
| C 14 | 257.4 | 3.4 | 14796 | 4 | US-09-496-694B-3 | | Sequence 3, Appl |
| 15 | 254.6 | 3.4 | 588 | 4 | US-09-385-982-128 | | Sequence 128, App |
| 16 | 254.6 | 3.4 | 176373 | 5 | US-09-128-155-17 | | Sequence 17, Appl |
| 17 | 253.4 | 3.4 | 4517 | 5 | PCR-US93-06251-83 | | Sequence 83, Appl |
| C 18 | 253 | 3.4 | 2373 | 4 | US-08-975-762-45 | | Sequence 45, Appl |
| C 19 | 253 | 3.4 | 2373 | 4 | US-09-293-028-45 | | Sequence 45, Appl |
| C 20 | 253 | 3.4 | 2373 | 4 | US-09-106-582-45 | | Sequence 45, Appl |
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| C 22 | 252.8 | 3.4 | 15328 | 2 | US-08-888-497-33 | | Sequence 33, Appl |
| C 23 | 252.8 | 3.4 | 15328 | 4 | US-09-362-230-33 | | Sequence 33, Appl |
| C 24 | 252.8 | 3.4 | 15328 | 5 | PCR-US94-07926-33 | | Sequence 33, Appl |
| C 25 | 250.6 | 3.3 | 59065 | 4 | US-09-813-817-3 | | Sequence 3, Appl |
| 26 | 250 | 3.3 | 72604 | 4 | US-08-268-992-7 | | Sequence 7, Appl |
| C 27 | 249.6 | 3.3 | 22481 | 4 | US-08-367-811A-43 | | Sequence 43, Appl |

ALIGNMENTS

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RESULT      1
US-09-173-914-6
; Sequence 6, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Eric
; TITLE OF INVENTION: A No. 6171857el Leucine zipper, KARP-1 and
; FILE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
; FILE REFERENCE: H0877/7017/HK
; CURRENT APPLICATION NUMBER: US/09/173,914
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 60/064,557
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 14636
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-173-914-6

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| Best Local Similarity | 90.5% | Pred. NO. | 1.1e-51 | | | | |
| Matches | 286 | Conservative | 0 | Mismatches | 30 | Indels | 0 |
| Gaps | 0 | | | | | | |
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| QY | 4815 | ggcatctgtgctcactgcgaagctgcctctgcctgggttcacgcgcaattctctgcctcagcc | 4874 | | | | |
| Db | 12296 | gggatactgcgtcactgcgaagtcgcctcccggttcacgcgcaattctctgcctcagcc | 12355 | | | | |
| QY | 4875 | ttccaatagctgggattgcaggatccacaacacaccggctaatatttttgtattttt | 4934 | | | | |
| Db | 12356 | tcccaagtgtgggtactacaggcgccgcctacgcgggtcaatttttgtattttt | 12415 | | | | |
| QY | 4935 | agtagacaggggtttccacatgttaccaggtatgacatgggtctgtatctctgcactgtaac | 4994 | | | | |
| Db | 12416 | agtagacaggggtttccacogtttttagccggatgggtctgatctctgcactgctgac | 12475 | | | | |
| QY | 4995 | tgcctgcctgcctcccaaatgctgggattacaggtgtgagccacogtgcctgggcaa | 5054 | | | | |
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RESULT 5
US-08-629-939-5

RESULT 6
US-08-759-873-5
; Sequence 5, Application US/08759873

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 16:43:00 ; Search time 7392.1 Seconds
(without alignments)
13686.662 Million cell updates/sec

Title: US-09-715-927-7
Perfect score: 7496
Sequence: 1 agctggctcaggcgctccgc.....gttaggcagtgaaaaaaa 7496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
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16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 603.8 | 8.1 | 875 | 10 BG536539 | BG536539 602564946 |
| c 4 | 598.6 | 8.0 | 913 | 9 AL543564 | AL543564 AL543564 |
| 5 | 579.6 | 7.7 | 911 | 10 BF574374 | BF574374 602131579 |
| 6 | 543.4 | 7.2 | 631 | 10 BG924298 | BG924298 HNC26-1-D |
| 7 | 519.2 | 6.9 | 810 | 9 AU133566 | AU133566 AU133566 |
| 8 | 519.2 | 6.9 | 896 | 9 AU505078 | AU505078 AU505078 |
| 9 | 505.6 | 6.7 | 771 | 9 AU134630 | AU134630 AU134630 |
| 10 | 500.6 | 6.7 | 618 | 9 AW963336 | AW963336 EST375409 |
| 11 | 496.2 | 6.6 | 732 | 10 BI835465 | BI835465 603087579 |
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18 453 6.0 3071 11 AK008700
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c 21 443.8 5.9 586 10 BG689712
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23 432.4 5.8 567 10 BG942981
c 24 431.8 5.8 456 9 AI248642
c 25 425.2 5.7 481 9 AW167802
c 26 425 5.6 433 9 AU139532
c 27 421.6 5.6 726 9 AU138245
c 28 419.8 5.6 448 9 AW450389
c 29 418.6 5.6 665 9 BB623179
c 30 418 5.6 443 9 AI127313
c 31 414.2 5.5 434 9 AI874113
c 32 410.6 5.5 565 10 W23461
33 406.4 5.4 439 9 AL559331
34 404 5.4 987 9 AL551987
35 403.4 5.4 431 9 AA226177
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c 38 387 5.2 425 9 AA226521
c 39 383.4 5.1 752 10 BI158667
c 40 375 5.0 759 9 AL572951
41 363.4 4.8 434 10 D82422
42 349 4.7 349 9 AA386154
43 348 4.6 515 10 D63209
44 347 4.6 563 9 AA490669
45 341.2 4.6 603 10 BI460172

ALIGNMENTS

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DEFINITION RC4-BT0311-250200-014-b06 BT0311 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE069938
VERSION BE069938.1 GI:8409134
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663

JOURNAL

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

COMMENT

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC4-BT0311-250200-014-b06&st3=2000-02-25&st4=1)
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High quality sequence start: 16
High quality sequence stop: 623.
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/dev_stage="Adult"
/clone_lib="B70311"
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
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Best Local Similarity 99.5%; Pred. No. 1.2e-74;
Matches 616; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 504 AACCAGCCTGTGTTCTGGCTGGCATGGCTGTGCTTCTTTATATGACTGCTCCTGGGC 445
QY 5595 tttagactcaccacacaggggtacccctacacacagggagctgagtggttccatccatcagt 5654
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ACCESSION AUI37852
VERSION   AUI37852.1 GI:10999373
KEYWORDS  EST.
SOURCE    human.
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
AUTHORS    Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE      HRI human cDNA project
JOURNAL    Unpublished (2000)
COMMENT    Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana-Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Best Local Similarity 98.3%; Pred. No. 2.1e-74;
Matches 628; Conservative 0; Mismatches 9; Indels 2; Gaps 1;
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Best Local Similarity 97.6%; Pred. No. 1.5e-72;
Matches 616; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

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RESULT 5
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ACCESSION BF574374
VERSION BF574374.1 GI:11648086
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 911)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LICM1082 row: n column: 20
High quality sequence stop: 632.

FEATURES
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/lab_host="NIH_MGC_81"
/note="Organ: muscle (T1 phase-resistant)"
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and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

BASE COUNT 214 a 222 c 228 g 247 t
ORIGIN

Query Match 7.7%; Score 579.6; DB 10; Length 911;
Best Local Similarity 97.2%; Pred. NO. 5.7e-70;
Matches 632; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

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Db 436 TGTATTCAATGCTGGAAACCCCTGAGACTTGTCCGTTTCTCTCTTTTGAAGATATCCGATC 495
|:|||||||||
QY 5855 aaggttcattcaagagagtgcaattacacctaccagataacctgaaattacaaactgaaat 5914
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Db 496 AAGGTTTCAATCAAGGAGAGTCAATTACACCTACCAAGATACCTGAAA-TACAACATGAAAT 554
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QY 5915 atacatgctaatgggtcttaattctgtcttaattgtcccgagagacaagtctcctgaatcgt 5974
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|:|||||||||
QY 5975 gcccataatctctgactgctgtgttgcagggcctcatttgcgtctagaa 6024
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Db 614 GGCCATAATCTCTGTCTGCTGCTGTTTGCAGGCGTCTATTCCTGCTAGNA 663
|:|||||||||

| | |
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| RESULT | 6 |
| BG924298 | 631 bp mRNA linear EST 06-NOV-2001 |
| LOCUS | HNC26-l-Dl.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA |
| DEFINITION | HNC26-l-Dl.R HNC (Human Normal Cartilage) sequence. |
| ACCESSION | BG924298 |
| VERSION | BG924298.1 GI:14318821 |
| KEYWORDS | EST. |
| SOURCE | human. |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 631) Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W. |
| TITLE | Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries |
| JOURNAL | Osteoarthritis Cartilage 9 (7), 641-653 (2001) |
| MEDLINE | 21482651 |
| COMMENT | Contact: Sanjay Kumar UW2109 GlaxoSmithKline 709 Swedeiland Road, P.O. Box 1539, King of Prussia, PA 19406, USA Tel: 610-270-7245 Fax: 610-270-5598 Email: sanjay_kumar-1@gsk.com Seq primer: T7 |
| FEATURES | Location/Qualifiers 1..631 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HNC (Human Normal Cartilage)" /tissue_type="cartilage" /lab_host="E.coli DH10 B" /note="Vector: pSPORT I"; Site_1: SalI; Site_2: NotI; Directional" |
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| Query Match | 7.2%; Score 543.4; DB 10; Length 631; |
| Best Local Similarity | 99.6%; Pred. No. 5.6e-65; |
| Matches 544; Conservative | 0; Mismatches 2; Indels 0; Gaps 0; |
| QY 6717 atcagaaaaaacagaactaaagaagtgttgataggactctcttttgtctgtagactgt 6776 | |
| Db 86 ATCAGAAAAAACAGACTAAGAAGTTGTGTAGATTAGACTTCTTTTTGTCGTGACTGT 145 | |
| QY 6777 aaaaatcattttagggccactaataccacaattatttatgaataaataattcttaa 6836 | |
| Db 146 AAAATCATTTATTGAGGCCACTAATAACCAATATTTATTATGAATAAAATTCCTTAA 205 | |
| QY 6837 ggcaaggtatcggtatatatttaagdtgcacttaaacacagtcaggctgaataatgatattttg 6896 | |
| Db 206 GGCAAGGCTATGGTGATATTTTAAGGTGACTTAAAGACAGTCAGGCTAAAATCTATATTTTG 265 | |
| QY 6897 catatgtcaacagattttttatctgtgatttgaaatgatgtgcgtgaactaaaatctaatt 6956 | |
| Db 266 CATATGTCAACAGATTTTTTATCTGTGATTTGAAATGTATGCGCTGTAAACTAAAAATCTAAT 325 | |
| QY 6957 cttaaaaaataatttattatagctctttgttccttggattttaactgtgacacagttgc 7016 | |
| Db 326 CTTTAAAAAATAATTTATTATTAGCTCTTTGGTCCCTTTGATTAACTGTGCACAGATGC 385 | |
| QY 7017 tgcaagaaaaatgtaattgaaatctgaagaggcattataaaatgggtgcacagaacctccaatga 7076 | |
| Db 386 TGCAAGAAAAATGTAATTGAATCTGAAGAGGCATTATATAAATGGGTGACAGAACTCCATGA 445 | |
| QY 7077 actatctcttgatctcttgcatctcatcaatcgtgcatcctggctccaaatcctgaagctt 7136 | |
| Db 446 ACTATCTCTTGATCTTCTGCAATTCATCATGGTTCATCTGGCTCCCAATCCTGAAGCTT 505 | |

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| Qy | 7137 | ttgcttgctcgtattgatttcagtcctctcttggcgaatggcgccacatgatgtattcc | 7196 |
| Db | 506 | TTGGCTTCTCGTATTGATTTTCAGTCTCCTTTGGCAATGGCCACATTATGTTATTC | 565 |
| Qy | 7197 | gatttgcacaaatactctgggaacaaagctcttttggcggctcctgatgcacaaagaag | 7256 |
| Db | 566 | GATTGGCCAAAATACTCTGGGAACAAGCTCTTTGGTAGCGGCTCTGATGCANAGAAG | 625 |
| Qy | 7257 | ttagga 7262 | |
| Db | 626 | TTAGGA 631 | |
| RESULT | 7 | | |
| LOCUS | AUI133566 | 810 bp | linear |
| DEFINITION | AUI133566 OVAR1 Homo sapiens cDNA clone OVARC1000166 5', mRNA | | EST 24-OCT-2000 |
| ACCESSION | AUI133566 | | |
| VERSION | AUI133566.1 | GI:10994105 | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | |
| | 1 (bases 1 to 810) | | |
| | Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., | | |
| | Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and | | |
| | Isogai,T. | | |
| TITLE | HRI human cDNA project | | |
| JOURNAL | Unpublished (2000) | | |
| COMMENT | Contact: Takao Isogai | | |
| | Genomics Laboratory | | |
| | Helix Research Institute | | |
| | 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan | | |
| | Tel: 81-438-52-3951 | | |
| | Fax: 81-438-52-3952 | | |
| | Email: genomics@hri.co.jp | | |
| | HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix | | |
| | Research Institute; cDNA library construction: Department of | | |
| | Virology, Institute of Medical Science, University of Tokyo, and | | |
| | Helix Research Institute. | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..810 | | |
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| | /clone_lib="OVARC1" | | |
| | /tissue_type="ovary, tumor tissue" | | |
| | /note="Vector: pHE18SFL3" | | |
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| Best Local Similarity | 99.4%; | Pred. No. 1e-61; 3; Indels 0; Gaps 0; | |
| Matches 521; Conservative | 0; Mismatches | | |
| Qy | 6973 | tattatagctcttggctcttggatttaactgtgacacagttgctgcaagaaaatgtaat | 7032 |
| Db | 58 | TAGATTCGGTCTTGGTCTCTTGGATTAACTGTGCACAGTTGCTGCAAGAAATGTAAT | 117 |
| Qy | 7033 | tgaatctgaaagagcattataaattgggtgtacagaactccatgaactatctcttgatct | 7092 |
| Db | 118 | TGAATCTGAAAGAGGCATTATAAATGGTGTACAGAACTCCATGAATCTCTCTTGATCT | 177 |
| Qy | 7093 | ctgcattctcatggtcattccctggctccaaatccctgaagcttttgcttgcgtatt | 7152 |
| Db | 178 | TCTGCATTTTCATCATGGTGCATCCCTGGCTCCAAATCCTGAAGCTTTTGGCTTGGCTGCTATT | 237 |
| Qy | 7153 | gatttcagctctccttggcgaatggcgccacattatgtatttcgcgatttggccaaaatac | 7212 |

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Db 238 GATTTTCAGTCTCTTTGTGGCAATGGCCACACATATGTAATTTCCGATTTGCCCAAAATAC 297
QY 7213 tctgggaacaagctcttctgctgcgtctgatgcaaaagaagtttagaagaaaaatca 7272
Db 298 TCTGGGAACAAGCTCTTTGCTTGGCGTCTCTGATGCAAAAGAAAGTTAGGAAGGAAAATCA 357
QY 7273 agcaataacatctgttctgttgagacagtttaactgtgtctatctctgttactagattatat 7332
Db 358 AGCAATATACATCTGTTTGTGACAGAGTTAACTGTGTCTATCTCTTACTAGATTATAT 417
QY 7333 agagcacatgtcttatttcttactcagaattcccaataaagctgttgagaaacctaaagtcagcaga 7392
Db 418 AGAGCACATGTGCTTAATTTGTACTCCAGAAATCCAAATAAATGGCTGCGGTGTTTCTCT 477
QY 7393 gttttaccacagctgtgccttgagaaactaaagctgtttaggaaacctaaagtcagcaga 7452
Db 478 GTTTTACCACAGCTGTGCTTGAGAACTAAAGAGCTGTTTAGGAACCTAAAGTCAGCAGA 537
QY 7453 aattaactgataatttccttctatgttgaggcatggaataaaaaa 7496
Db 538 AATTAAGTATTAATTTCCCTTATGTGTGAGGCATGGAAAAAAA 581

RESULT 8
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LOCUS AL550578 LTI_NFL006_PL2 896 bp mRNA linear EST 16-FEB-2001
DEFINITION AL550578 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI058Y22 5
prime, mRNA sequence.
ACCESSION AL550578
VERSION AL550578.1 GI:12887677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Li,W.B., Gruber,C., Jessee,J. and Pollayes,D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
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/clone="CSODI058Y22"
/tissue_type="placenta"
/Note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 265 a 155 c 165 g 310 t 1 others
ORIGIN

Query Match 6.9%; Score 519.2; DB 9; Length 896;
Best Local Similarity 99.4%; Pred No. 1e-61;
Matches 521; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6973 tattatagctcttggctcttgatttaactgtgacacagttgctgcaagaaaatgtaat 7032
Db 51 TAGAATCGGTCTTTGCTCTCTTGTATTAAGTCTGACACAGTTGCTGCAAGAAAATGTAAT 110
QY 7033 tgaatctgaagaggcattataaattgggtgacagaactccatgaaactatcttcttgatct 7092

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Db 111 TGAATCTGAAAGAGGAGTATAAATGGTGTACAGAACTCCATGAACATATCTTCTGATCT 170
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Db 171 TCTGCATTTTCATCATGCTCATCTGCTGCCATCCAAATCCTGAAGCTTTTGGCTTGGCTCGTATT 230
QY 7153 gatttcagtcctccttctgtgcaatggcgccacattatgtatttcccgatttgcgcaaaatcac 7212
Db 231 GATTTTCAGTCTCTCTTTGTGGCAATGGCCACACATATGTAATTTCCGATTTGCCCAAAATAC 290
QY 7213 tctgggaacaagctcttctgctgcgtctgatgcaaaagaagtttagaagaaaaatca 7272
Db 291 TCTGGGAACAAGCTCTTTGCTTGGCGTCTCTGATGCAAAAGAAAGTTAGGAAGGAAAATCA 350
QY 7273 agcaataacatctgttctgttgagacagtttaactgtgtctatctctgttactagattatat 7332
Db 351 AGCAATATACATCTGTTTGTGACAGAGTTAACTGTGTCTATCTCTTACTAGATTATAT 410
QY 7333 agagcacatgtcttatttcttactcagaattcccaataaagctgttgaggctgggtgttctctct 7392
Db 411 AGAGCACATGTGCTTATTTTGTACTGCAGAAATCCAAATAAATGGCTGGGTGTTTCTCTCT 470
QY 7393 gttttaccacagctgtgccttgagaaactaaagctgtttaggaaacctaaagtcagcaga 7452
Db 471 GTTTTACCACAGCTGTGCTTGAGAACTAAAGAGCTGTTTAGGAACCTAAAGTCAGCAGA 530
QY 7453 aattaactgataatttccttctatgttgaggcatggaataaaaaa 7496
Db 531 AATTAAGTATTAATTTCCCTTATGTGTGAGGCATGGAAAAAAA 574

RESULT 9
AL134630 Homo sapiens
LOCUS AL134630 PLACE1 771 bp mRNA linear EST 24-OCT-2000
DEFINITION AL134630 PLACE1 Homo sapiens cDNA clone PLACE1000166 5', mRNA
sequence.
ACCESSION AL134630
VERSION AL134630.1 GI:10995169
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
JOURNAL HRI human cDNA project
COMMENT Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
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/lab_host="DH10B"
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source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: This is a NIH_MGC Library."
211 a 134 c 146 g 241 t

BASE COUNT      279 a 181 c 183 g 212 t
ORIGIN

Query Match      6.6%; Score 496.2; DB 10; Length 732;
Best Local Similarity 99.0%; Pred. No. 1.5e-58;
Matches 520; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Qy 7092 ttctgcatttcacatcgtgctcctggtcctccaaatccctgaagcttttggcttgcgtat 7151
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Qy 7152 tgatttcagtccttttggcaatggccacattatgtatttcogattttgccccaaaaa 7211
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Qy 7212 ctctgggaacaagctcttctgctgctgctgacgaaagagtttaggaagaaatc 7271
Db 289 CTCGGGAACAAAGCTCTTCTGCTGGCTCTGATGCAAAAGAGTTAGGAGGAAATC 348

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Qy 7392 tgtttttaccacagctgtgccttgagaaactaaaagctgttttagaaacctaaagtcagcag 7451
Db 469 TGTTTTTACCACAGCTGTGCTTGAGAACTAAAGCTGTTTAGGAAACCTAAGTCAGCAG 528

Qy 7452 aaattaactgattaattcccttattgttgagggcatggaaaaaaa 7496
Db 529 AAATTAAGTGATTAATTTCCCTTATGTTGAGGCATGGCAAAAAA 573

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DEFINITION AL577308 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0DI083YA09 3
prime, mRNA sequence.
ACCESSION AL577308
VERSION AL577308.1 GI:12940310
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)

```

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
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/tissue_type="placenta"
/vector="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
cloned, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 279 a 181 c 183 g 212 t
ORIGIN
Query Match 6.6%; Score 494.4; DB 9; Length 859;
Best Local Similarity 89.1%; Pred. No. 2.5e-58;
Matches 531; Conservative 2; Mismatches 63; Indels 0; Gaps 0;
Qy 5529 tactacaaccgctgtttctggctgcatgggtctgtcttcttcttcttatatgactgc 5588
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Qy 5589 ctgggctttagctcatcaccacaggggtacgcctacactcagggaactgagtggttccatc 5648
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Db 679 TGGCTACGTCGAAATGTTGGTTGGTTCGGACAGCTCTGATCTCAGGATTTGGCAGAGCTT 620
Qy 5769 tctgtttgactgtgtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 5828
Db 619 TCCTGTTTGTATCTTGTGTGTATCTCTGATTCATGCTGGAAGCCCTGGACTGTGTC 560
Qy 5829 gttctccttttgaagatatccgcatcaagggttcattcgaagagagcagcagcagcagcagc 5888
Db 559 GTTTCTCCTTTTGAAGATATCCGATCAAGGTTTCAATCAAGGAGAGTCAATTAACACTACC 500
Qy 5889 aagatcacctgaaattacaactgaaatacacatgtcctaagtggtctaaattctgctaaatt 5948
Db 499 AAGATACCTGAAATTAACACTGAAATATACATGCTAATGGGTCTAATTCGCTAATATT 440
Qy 5949 gtcccgagacagaactcctgaaatcctgtgccccataatcctgtcagctgctgtgttgagcagc 6008
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Db 379 GTCATGCTGCTAGAATCGGTCCTTTGGTCCCTTGTATTAACTGTGACACAGTTGCTGCAA 320
Qy 6069 ttgtgtaatgtaggttcagagaatccattataataatgctgaaatgttctccta 6124
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| Db | 329 | ACAGAACTCCATGAACATATCTTCTTGATCTCTCTGATTTTCATCATGGTCATCTCGGCTCC | 270 |
| Qy | 7123 | aaatcctgaagcttttggcttgcctgattgattcagtcctcttggcaatggagcca | 7182 |
| Db | 269 | AAATCCCGAAGCTTTGGCTTGCCTGCGTATGATTACGTCCTCTTGGCAATGGGCCA | 210 |
| Qy | 7183 | cattatgtattcttcgatttggccaaaataactctctgggaaaaaagctctcttcttgcggtcc | 7242 |
| Db | 209 | CATTATGTATTTCGGATTTCGCCAAATACTCTGGGAAACAAGCTCTTTGCTTGGCGTCC | 150 |
| Qy | 7243 | tgaatgcaaaagaaattaggaagaaatacaagcaaaatcacatctgttcttggagacaqttt | 7302 |
| Db | 149 | TGATGCAAAAGAACTTAGGAAGGAATATCINAGCGNAATACATCTATCAAAAGAGACAGTTT | 90 |
| Qy | 7303 | aactgttctcatcctgttaactagattatataagacacatgtcttattttgt | 7354 |
| Db | 89 | AACTGTTGCTATCTGTACTAGATTATATAGACACATGTGCTATTNNVGT | 38 |
| RESULT | 14 | | |
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| DEFINITION | 602645928F1 NIH_MGC_76 | Homo sapiens cDNA clone IMAGE:4767414 | 5', 3' |
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| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| AUTHORS | NIH-MGC | http://mgc.nci.nih.gov/. | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| JOURNAL | Unpublished (1999) | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI629 row: h column: 07 High quality sequence stop: 724. | | |
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| | /clone_lib="NIH_MGC_76" | | |
| | /lab_host="DH10B (TI phage-resistant)" | | |
| | /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccattcgcc); Site_2: SfiI (ggccattcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A, C, G or N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library." | | |
| BASE COUNT | 212 a | 131 c | 147 g 237 t |
| ORIGIN | | | |
| Query Match | 6.5% | Score 488; | DB 10; Length 727; |
| Best Local Similarity | 99.6% | Pred. No. 2e-57; | |
| Matches 510; | Conservative | 0; Mismatches | 0; Indels |
| | | | 2; Gaps |

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QY 7045 aggcattataaattggtgtacagacccatgaactatctcttgatctcttcgattctat 7104
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QY 7465 aatttccttattgtgagcatgggaaacaaaaa 7496
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RESULT 15
AV704855 731 bp mRNA linear EST 09-OCT-2000
DEFINITION AV704855 ADB Homo sapiens cDNA clone ADBCD11 5', mRNA sequence.
ACCESSION AV704855
VERSION AV704855.1 GI:10722167
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 731)
Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao
, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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FEATURES
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Best Local Similarity 96.2%; Pred. No. 1.2e-56;
Matches 504; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
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Db 107 TAGAATCGGTCTTTGGTCTCTTTGATTTAACTGTGACACAGTTGCTGCAAGAAATGTAAT 166

QY 7033 tgaactctgaaagagcattataaattgggtgtacagaaactccatgaactatcttcttgatct 7092
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QY 7093 tctgcaattcactcaggttcactcctcctgctcccaatcctcgaagcttttggcttgcctcgtat 7152
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